PRELIMINARY PROPOSAL FOR FY2005 FUNDING

Title: Mechanisms of delayed mortality in juvenile salmonids outmigrating in the Columbia River Basin

4. Study codes: BPS-W-05-01 (new)

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PROJECT SUMMARY

RESEARCH GOALS

The goal of this study is to explore the influence of two probable mechanisms (i.e., increased vulnerability to disease and predation) of delayed mortality of transported or bypassed juvenile salmonids migrating below Bonneville Dam. The results of this study will inform managers of the ultimate causes of delayed mortality. This information can be considered when making management decisions about operation of the Columbia River hydropower system, including the transportation and spill programs.

STUDY OBJECTIVES

Objective 1. Assess the vulnerability to predation of juvenile spring Chinook salmon that have been barged and those that have experienced different bypass histories during their in-river migration.

Passage of juvenile salmonids through or around the Columbia River Basin (CRB) hydrosystem exposes fish to numerous, possibly cumulative, stressors. Examples of stressors include handling and dewatering, passage through bypass systems at dams, loading, crowding and unloading from barges, and exposure to elevated temperatures and contaminants. Exposure to these stressors may lead to delayed mortality of fish that occurs during the estuary or ocean life stage. This delayed mortality may claim 37 to 68% of juvenile salmon that pass Bonneville Dam (Budy et al. 2002). Also, delayed mortality occurrence may differ for hatchery and wild fish, and for fish that have been transported compared to fish that migrated in-river. The ratio of smolt-to-adult survival comparing transported and inriver migrants (D) may be < 1.0, suggesting delayed mortality of transported fish (Budy et al. 2002). Ultimately, delayed mortality could lead to reductions in smolt-to-adult survival rate and reduce the number of recruits per spawner.

We will conduct laboratory and field experiments with spring Chinook salmon designed to explore the relative seriousness of increased vulnerability to predation as a contributing mechanism of delayed mortality. This research will use well-established and powerful predator-prey bioassays in seawater systems to determine the vulnerability of different groups of fish to predation by common estuarine or marine predators.

Objective 2. Assess the physiological and health status of juvenile spring Chinook salmon that have been barged and those that have experienced different bypass histories during their in-river migration.

We will use new technologies, such as real-time quantitative polymerase chain reaction (qPCR) and salmonid-specific cDNA microarrays, to document the health and physiological status of different groups of fish at Bonneville Dam. The cDNA microarray will identify genes that are differentially turned on or off, and will point to physiological systems (e.g., osmoregulation, stress, metabolism, immunity) that may be impacted by route of migration of the fish. Using these techniques, we will also identify and develop molecular probes that are sensitive and reliable indicators of stress and fish health. Such information will provide much needed insight into whether disease, behavioral or developmental dysfunction may contribute significantly to delayed mortality in different groups of fish. Similar methodologies were used to identify the physiological processes that allow fish to survive fluctuating daily water temperatures (Prodrabsky and Somero 2004), and the effects of contaminants on fish in

laboratory and field studies (Hogstrand et al. 2002; Williams et al. 2003).

RELEVANCE TO BIOLOGICAL OPINION

The Objectives of this proposal are relevant to Reasonable and Prudent Alternatives (RPAs) 5, 7 and 16, and Conservation Recommendation 2 in the NMFS 1995 Biological Opinion for Operation of the Federal Columbia River Power System (RCRPS), and in Terms and Conditions 1.j, 1.k, 2.d, 2.f, and 2.h in the 1998 Supplemental Biological Opinion. Addressing the relations between delayed mortality and hydropower operations is a critical factor in the 2000 FCRPS Biological Opinion RPAs, as indicate in Section 9.6.1 (page 9.4):

> "In hydro, for example, the projected effect of the hydro measures, or of the alternative of breaching dams, depends largely on the degree to which there is delayed mortality associated with juvenile fish passage at those dams, either inriver or with barge transportation, and the degree to which that delayed effect would be mitigated with breaching of any particular dam or dams."

This proposal addresses many RPAs in the 2000 FCRPS Biological Opinion. Specifically, RPAs 45, 46, and 47 under Section 9.6.1.3 Juvenile Fish Transportation require studies to address delayed mortality as the result of transportation. Moreover, virtually all of the RPAs in Section 9.6.1.4 Fish Passage (RPAs 54 through 98) address evaluations of operations and modifications of the FCRPS with the goal of increasing smolt-to-adult survival (i.e., decreasing delayed mortalities).

PROJECT DESCRIPTION

BACKGROUND AND JUSTIFICATION

The Pacific Northwest is currently in the midst of an unprecedented decline of many stocks of anadromous salmonids. This crisis has precipitated tremendous amounts of research and management action aimed at trying to halt or reverse this decline. One factor potentially limiting salmonid production in the CRB is delayed mortality of juvenile fish after they have passed Bonneville Dam and entered the estuary and ocean. Delayed mortality, as defined by Budy et al. (2002), refers to mortality of fish that occurs in the estuary or ocean that is related to their earlier experiences in the hydrosystem. For example, fish may die in the estuary after leaving the hydrosystem (below Bonneville Dam) as a result of numerous, possibly cumulative stressors they experienced after passing as many as eight dams. The proximate causes, or specific mechanisms, of delayed mortality are speculative, but exposure of fish to hydrosystem-related stressors may make them more vulnerable to predation (see Mesa 1994) in the marine environment or lead to clinical expression of disease. *Renibacterium salmoninarum*, the causative agent of bacterial kidney disease (BKD) and a focus of this proposal, is prevalent in salmonid out-migrants from the Columbia and Snake River basins (Sanders et al. 1992; Maule et al. 1996; Elliott et al. 1997). Although evidence exists that anadromous salmonids infected with *R. salmoninarum* while in freshwater may die of BKD during downstream migration (Pascho et

al. 1993) or after entry into seawater (Banner et al. 1986; Sanders et al. 1992; Elliott et al. 1995), more information is needed on the incidence and severity of BKD in fish with different bypass histories to better link BKD with delayed mortality. In addition, little is known about the possible contribution of other fish pathogens to delayed mortality.

Recently, a workshop was convened by the Comparative Survival Study Oversight Committee and the U. S. Fish and Wildlife Service to organize and integrate the scientific information on the indirect effects (i.e., delayed mortality) of hydrosystem configuration and operation on salmon and steelhead survival. One conclusion of this workshop was that increased vulnerability to predation and disease were likely contributors to delayed mortality, but confirmatory evidence for this hypothesis was lacking. Specifically, information is needed on whether mechanisms of delayed mortality may be differentially affecting groups of fish with different bypass histories. Budy et al. (2002) demonstrated an almost 2-fold greater smolt-to-adult survival (SAR) of summer and spring Chinook salmon that were not bypassed or bypassed at one dam as compared to those bypassed at two or more dams. These differences raise many questions about causality, for example, are there differences in vulnerability to predation or disease among fish that were: (1) never detected in a bypass system, (2) detected one or more times, or (3) barged around the dams? Determining the answer to this question will certainly increase our understanding of the effects of hydrosystem passage on delayed mortality of juvenile salmonids and is the focus of our proposal.

Mortality of juvenile salmonids migrating to the ocean in the CRB can be divided into two broad categories: direct and indirect, or delayed, mortality. Direct mortality is mortality that is measurable and occurs within the hydrosystem, i.e., at or upstream of Bonneville Dam. Some examples of direct mortality might include mortality that occurs during turbine passage or is attributable to predators feeding in the slack-water reservoirs. Delayed mortality, in contrast, is mortality that occurs during the estuarine or ocean phase of juvenile salmon and can be attributed to earlier hydrosystem experiences. For example, fish migrating through several dams on the Columbia River might be exposed to multiple, cumulative stressors that manifest themselves as an increased vulnerability to predation in the marine environment. Thus, exposure to stressors occurs during passage through the hydrosystem, but mortality occurs sometime later when fish are in the estuary or ocean. Currently, delayed mortality of juvenile salmonids, as defined here, seems to be more of a theoretical idea because little direct evidence exists to document its occurrence. Budy et al. (2002) argue that SARs of various groups of fish that experience different passage routes during their migration in the CRB is direct evidence of delayed mortality. For example, SARs of juvenile fish that migrated in-river and went through three or more bypass systems at different dams (assumed to be relatively stressful) were lower than SARs of fish that never got detected in a bypass system. Presumably, fish that did not get detected at various bypass systems passed the dams via the more natural, less stressful route of spill, thus minimizing delayed mortality and leading to an increase in SARs.

There is, however, a plethora of indirect evidence supporting the existence of delayed mortality and Budy et al. (2002) provide an excellent summary of this topic. Much of the indirect evidence for the existence of delayed mortality revolves around the impact of stress on

fish and is based on a voluminous literature. Figure 3 in Budy et al. (2002) summarizes it this way: (1) juvenile fish can migrate past a dam as many as eight times; (2) fish passing a dam will either die, experience no effect, or be exposed to stress; (3) if exposed to stress, fish may recover completely, as in an acute physiological stress response, or they may experience cumulative or chronic effects; (4) cumulative or chronic effects of stress can lead to poor health, diminished physical abilities, and, presumably, delayed mortality.

The problem with much of this evidence, however, is that it was not generated with the specific objective of evaluating delayed mortality. For example, much of the literature on stress in fish results from trying to understand the effects of aquaculture-related stressors on fish physiology and health. Thus, although such work can contribute to a theoretical and physiological framework for understanding the potential of stress to elicit delayed mortality in fish, it seems to be an incomplete surrogate for actual experimentation addressing the specific issue of delayed mortality. Does passage through several dams lead to metabolic or immune dysfunction and increased vulnerability to disease? Does passage through several dams compromise the physical abilities of fish to a point where they may be more vulnerable to predation in the marine environment? To our knowledge, studies addressing these specific questions have not been conducted, despite their obvious contributions to our understanding of the effects of stress on fish and delayed mortality. One of the reasons for the paucity of information may be due to the lack of sensitive and reliable indicators of longer-term (chronic) stress in fish. Most of the commonly used end-points of stress (such as plasma cortisol, glucose and lactate levels) are highly variable and influenced to a large extent by the immediate stressful activity. Consequently, these plasma end-points of stress provide limited information about the stress history (e.g., different passage routes) of the animal.

For this research, we will conduct laboratory studies and field sampling to determine whether vulnerability to predation and increased susceptibility to disease contribute significantly to delayed mortality of juvenile salmonids. Test animals for this research will be fish collected at Bonneville Dam from several migration history groups, including fish that have not previously been detected in a bypass system, fish that have been detected one other time, fish detected more than two other times, and those that have been barged. Our predation experiments will be conducted in large seawater mesocosms and will be ecologically realistic because they address a scenario that juvenile salmon probably encounter frequently in the marine environment. Sampling fish with different bypass histories at Bonneville Dam, which will include non-lethal methods, will provide documentation of their health and physiological status at the time of passage, requisite data for making predictions about the fate of fish in certain groups, and the ability to correlate health status of PIT-tagged fish with adult returns.

This research should provide much needed information regarding two probable mechanisms of delayed mortality in juvenile salmonids. The cutting-edge techniques proposed here have the potential to provide valuable insight into the health, well being, and physiological status of fish after they have been barged or passed through the hydrosystem. Also, these techniques will allow us to develop sensitive and reliable molecular tools with which to detect chronic stress in juvenile salmonids. Collectively, this work will help substantiate or refute

hypotheses concerning disease or predation, and perhaps lead to new hypotheses, as to the causes of delayed mortality in Columbia River juvenile salmonids. Identifying the causes of delayed mortality is the first step in understanding the phenomenon and will allow managers to make informed decisions when considering hydropower operations, including the transportation and spill programs

OBJECTIVES AND METHODOLOGY

Objective 1. Assess the vulnerability to predation of juvenile spring Chinook salmon that have been barged and those that have experienced different bypass histories during their in-river migration.

These experiments are designed to detect overt differences in predator avoidance ability between fish that have been barged and those that remained in-river during migration and experienced different bypass histories. On at least three occasions, we will collect fish at Bonneville Dam from different migration groups and subject them to predation bioassays in large, circular seawater microcosms located at the dam's artificial seawater facility. These large tanks will have flowing artificial seawater, structure in the form of rocks and woody debris, and will be in ambient photoperiod. Predators will be commonly encountered marine piscivores such as rockfish *Sebastes spp*., jack mackerel *Trachurus symmetricus*, or lingcod *Ophiodon elongatus*. Also, if necessary, experiments can be conducted using common freshwater predators, such as Northern pikeminnow *Ptychocheilus oregonensis* or smallmouth bass *Micropterus dolomieui*.

For these experiments, we will have 4-6 replicate predation tanks. We will collect 48 to 72 juvenile salmon from each of the following groups at Bonneville Dam using the sort-by-code system where appropriate: (1) barged; (2) nondetected at any other dam; (3) bypassed one time; and (4) bypassed two or more times. (Because fish will be collected at Bonneville Dam, all will have experienced at least one bypass system.) All fish will be briefly anesthetized using 50 mg/L tricaine methanesulfonate (MS-222) buffered with sodium bicarbonate and we will randomly select and mark three groups. All fish will be marked to identify groups by punching a small hole in the dorsal or anal fin or one of the paired fins. Marking procedures will rotate between groups for different sets of trials. After fish are marked, they will be transferred to the seawater facility and each group will be placed separately in four tanks containing fresh water.

One or two days after test-fish have been placed in freshwater, they will be gradually transitioned, over the course of a day, to full strength seawater. This 24-48 h holding in fresh water followed by a gradual change to seawater is meant to simulate environmental conditions during the migration from below Bonneville Dam to the estuary. After fish have transitioned to full strength seawater, 15 fish from each group will be water brailed simultaneously to the predation tanks. Predators will be allowed to consume juvenile salmon until 25-30% of the prey are eaten. We will observe fish behavior from overhead and estimate the number of prey eaten to determine when a trial should end. Afterwards, the remaining prey will be seined from the tanks and placed in a lethal dose (200 mg/L) of MS-222. Lengths and weights will be recorded and fish will be identified with a group depending on which mark they have. These experiments

will be conducted at least three times during the spring outmigration so the total number of fish sampled will be between 576 and 864 depending on how many predation tanks are available.

We will analyze these data in a manner identical to that of Mesa (1994). First, data will be subjected to a heterogeneity π^2 analysis to determine if the individual tests were homogenous (Sokal and Rohlf 1981). Chi-squared goodness-of-fit tests will then be used on pooled data to determine if predation was random (i.e., 25:25:25:25) on the different groups of fish. Because the π^2 test has low statistical power (i.e., low probability of correctly rejecting the null hypothesis) when relatively small sample sizes are used, we will set the significance level at 0.10, the detectable difference in predation rates (i.e., the effect size) at 20%, and target sample sizes at about 180 to increase power and reduce the probability of the more serious type II error (Fairbairn and Roff 1980, Peterman 1990).

Objective 2. Assess the health and physiological status of juvenile spring Chinook salmon that have been barged and those that have experienced different bypass histories during their in-river migration.

This work will involve sampling tissues from individuals in the groups described above to provide an indication of the general health and well-being of each population before leaving Bonneville Dam and migrating to the estuary. First, we will collect tissues from 15-20 fish in each group (lethal sampling) and assay them for various pathogens known to occur in the CRB, including the bacteria *R. salmoninarum*, *Yersinia ruckeri*, *Aeromonas salmonicida* and *Flavobacterium psychrophilum*, infectious hematopoeitic necrosis virus (IHNV), the myxosporean parasite *Ceratomyxa shasta*, and the microsporidian parasite *Nucleospora salmonis*. For detection of these pathogens, samples (25 mg minimum per sample) of kidney (two samples), gill, liver and intestine will be removed from each fish. A portion of the kidney will be placed in an RNA stabilization reagent for the IHNV assay. These stabilized samples can be held at 4°C for up to one week but will be transferred to –80°C for longer storage before processing and testing for IHNV RNA by reverse transcriptase-PCR (LaPatra et al. 2001). An additional kidney tissue sample will be preserved in 95% ethanol at room temperature for real-time quantitative PCR (qPCR) detection of *R. salmoninarum* (Elliott and Pascho 2004) and nested PCR detection of *Nucleospora salmonis* (Giorgiadis et al. 1998). A gill sample will also be preserved in ethanol and tested by quantitative PCR for *R. salmoninarum* for comparison with the non-lethal samples (see below). Liver tissue will be preserved in ethanol for detection of *Yersinia ruckeri*, *Aeromonas salmonicida*, and *Flavobacterium psychrophilum* by multiplex PCR (del Cerro et al. 2002). Intestinal tissue will also be preserved in ethanol for nested PCR detection of *Ceratomyxa shasta* (Palenzuela et al. 1999; Fox et al. 2000). We will conduct this sampling at least three times, so the total number of fish sampled will be 240.

At the same time as lethal samples are being taken, different fish from each group (N = 15-20) will be non-lethally sampled for gill tissue according to the method of Schrock et al. (1994), and preserved at room temperature in an individually numbered tube containing 95% ethanol. The PIT-tag and other pertinent information for each fish will be recorded and they will be released to continue their migration. Gill samples will also be tested for *R. salmoninarum* by

qPCR (Elliott and Pascho 2004). Documenting the health status of fish via non-lethal sampling could be useful for studying PIT-tagged fish and adult returns. It is possible that this non-lethal technique could be developed for other pathogens. Collectively, this information will provide an indication of the likelihood that fish from certain groups will develop clinical diseases during their estuary or ocean life stage. We will conduct this sampling at least three times, so the total number of fish sampled nonlethally will be 240.

cDNA microarray. We will use the same tissues collected during the lethal sampling of fish for the health assessment to determine the status of various physiological systems using a salmonid cDNA microarray. The advent of DNA microarray technology in the past decade has changed the face of physiological experimentation. The spotting of hundreds and thousands of genes on a single coated glass slide has opened up new possibilities in our ability to investigate and compare changes in genomic expression. Basically, cDNA microarrays are glass slides upon which are placed small segments of DNA that encode for genes associated with the production of specific biochemical products. For example, the 530 basepair (bp) segment of rainbow trout cDNA, hsp70i, encodes for the inducible form of heat shock protein 70, a product related to the cellular stress response. Heat and other stressors will increase the expression of this gene. Thus, by hybridization of RNA from various tissues on the cDNA microarray slide, we will be able to determine which genes, and therefore which physiological systems, are up- or down-regulated at the time of capture (for a detailed microarray protocol see Lou et al., 2001).

Dr. Vijayan's group has developed a targeted rainbow trout cDNA microarray for the detection of stressed states in fish (Wiseman and Vijayan, 2002; Lee et al., 2003). This cDNA microarray is unique in that it is made up of 150 trout genes that were cloned and sequenced from rainbow trout tissues [PCR-amplified cDNA fragments (450-550 bp) of trout genes (sequences available in GenBank)] that are well characterized and, therefore, functionally relevant. The primers for amplifying the cDNA fragments were designed by aligning all available sequences in the Genbank for each gene and picking the most conserved region. Consequently, this cDNA microarray also hybridizes nicely with other salmonids and, therefore, has wider cross-species applicability. These gene sequences have been grouped according to how their products relate to various physiological systems, including (1) stress physiology; (2) metabolism; (3) exposure to contaminants; (4) reproduction; (5) immune function and disease resistance; (6) osmoregulation or smoltification; (7) growth and development; and (8) respiration. Using this microarray, Dr. Vijayan's group has carried out studies on the gene expression profiles associated with different stress protocols in salmonids. The results from these studies clearly highlight the power of targeted microarrays for identifying genes or clusters of genes as reliable indicators of stress in fish. These results have been presented at several International meetings and will be submitted for publication in the coming weeks. The utility of cDNA microarray technology is immense and will be especially important for this proposal because it will provide not only insight into the physiological response to stressor exposure, but also will provide a tool to identify molecular probes that are indicative of homeostatic dysfunction associated with environmental stressors in the CRB. Such information could provide valuable insight into the physiological status of different groups of fish before they leave Bonneville Dam, would be useful for predicting the fate of fish as they continue their migration,

and could be used to develop testable hypotheses about the physiological basis of delayed mortality. Prodrabsky and Somero (2004) used microarray technology to identify physiological processes that allow an annual killifish (*Austrofundulus limnaeus*) to survive large daily fluctuations in water temperature (20 to 37º C). They were able to detect changes in the expression of genes the products of which are responsible for cell growth and proliferation, metabolic functions (e.g., carbohydrate, intermediary, and nitrogen metabolism), and immune responses.

SCHEDULE

Work on both objectives would start in the winter of 2005 with final experimental design, setup, and relevant purchasing. Predation bioassays and tissue sampling would occur during the outmigration of spring Chinook salmon, generally from about April through June 2005. Data proofing, analysis, and report preparation for our first year of work should be completed by December 2005. We propose that this study be repeated in 2006.

RELATIONSHIP OF PROPOSED RESEARCH TO OTHER ONGOING OR PROPOSED RESEARCH.

We are unaware of any similar delayed mortality work ongoing currently in the basin. Our proposed research should compliment past or future work on delayed mortality (e.g., the NOAA-Fisheries work of Gilbraith et al.).

IMPACTS

We anticipate that any impacts from this study on other ongoing or proposed research will be negligible. The total number of spring Chinook salmon to be sampled is from 816 to 1,104. We will nonlethally sample an additional 240 fish. We are unaware of any other biological impacts from this study.

LIST OF KEY PERSONNEL AND PROJECT DUTIES

Matthew Mesa, Principal investigator: oversight of predation studies, tissue sampling, analysis and writing

Alec G. Maule, Principal investigator: general project oversight, analysis and writing

Diane Elliott, Principal investigator: oversight of fish health studies, analysis and writing

Mathilakath (Matt) Vijayan, Principal investigator: oversight of DNA microarray studies, analysis and writing

FACILITIES AND EQUIPMENT

Predation work will be conducted at the artificial seawater facility at Bonneville Dam. Assays for this study will be conducted at the Columbia River Research Laboratory, the Western Fisheries Research Center in Seattle, and the University of Waterloo, Waterloo, Ontario, Canada.

All facilities are well supplied with all the modern equipment, computers, and analysis software necessary to complete this research.

The Columbia River Research Laboratory (CRRL) in Cook, WA, is part of the USGS's Western Fisheries Research Center (WFRC). The CRRL has three state-of-the-technology analytical laboratories dedicated to enzymology, immunology and cell culture, and general physiology. In addition to standard equipment such as centrifuges, pH meters, and balances, the laboratories are equipped with VIS-UV and reflectance spectrophotometers, enzyme-linked-immunosorbent assay (ELISA) plate readers, flame photometers, and ultracold freezers. The laboratory is staffed with trained technicians and biologists proficient in these techniques with backgrounds in fish behavior, immunology, physiology, and endocrinology. The 1500 sq. ft. wet lab facility is adequate to conduct various levels of investigation into fish development or behavior, including studies on disease resistance, reproduction, predator avoidance, thermal preference, osmoregulation, swimming performance and bioenergetics. The CRRL has a modern computer network that services over 100 users at the facility and a GIS laboratory. Computer software available for data analyses includes SAS, Excel, SigmaPlot, Statgraphics, and a variety of other word processing and data management software. The CRRL has its own T-1 line for fast Internet access.

The WFRC represents a state-of-the-art center for work on infectious diseases of fish that includes over 16,000 square feet of laboratory space for cell culture, virology, bacteriology, immunology, histology, parasitology, and molecular biology. The laboratory also houses a 9,000 square foot wet laboratory supplied with pathogen-free fresh water to 20 individual bays (each with temperature control from 4-25°C) containing a total of more than 300 tanks of various sizes. The laboratory effluent is treated with chlorine gas. Within the dry lab complex is a restricted access Biosafety Level 3 laboratory containing dry and wet laboratories for work with exotic fish pathogens. Also in the dry lab are a walk-in cold laboratory (4°C), walk-in cold storage (4 and -20°C), fluorescence microscopy rooms, a common computer room and an animal care facility meeting NIH guidelines. The laboratory is equipped with 2 ultracentrifuges, 4 refrigerated centrifuges, 4 refrigerated microfuges, automated equipment for enzyme-linked immunosorbent assays (ELISA), more than 10 PCR machines including an ABI 7900 sequence detection system, automated DNA sequencer, peptide synthesizer, DNA synthesizer, pulsed-field, protein, and nucleic acid electrophoresis equipment, 4 spectrophotometers, luminometer, fluorometer, scintillation counter, 5 chemical fume and 10 laminar flow hoods, 10 ultrafreezers, 5 research microscopes, networked and stand-alone computers with internet and both DNA and image analysis capabilities, and other large and small equipment items commonly found in microbiology and molecular biology laboratories.

Dr. Vijayan's laboratory at the University of Waterloo is well equipped for molecular biology and physiology research. His laboratory was recently awarded Canadian Foundation for Innovation and Ontario Innovation Trust grants to develop a state-of-the-art facility for biomarker development for stress detection in the aquatic environment. Some of the specialized equipment includes microarray scanner, qPCR, microplate readers for absorbance, fluorescence

and luminescence, epifluorescence microscope with imaging system, ultracentrifuge and electrophoresis system for proteomics.

TECHNOLOGY TRANSFER

Results from this study will be disseminated in the form of annual reports of research, oral presentations and briefings, and peer-reviewed journal publications.

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